

Operation: Present and Future

http://protein.nsls.bnl.gov



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Mission

The East Coast NIGMS Structural Biology Facility mission is to provide first class resources to the biological- biochemical-, and biophysics- communities to explore all aspects of structural biology. It is the goal of this facility to provide assistance to expert and non-expert crystallographers.

These goals include:

- Beam line access to a structural biology community at large.
- Fast access to beam time for the user community.
- Crystal screening and high-throughput data collection.
- Assistance and training for academic and professional users.



Background



- Beamline upgrades for benefit of general users
- Reports on increasing demand for user access and beamline needs
- Estimate of doubling of capacity for crystallographic experiments from staff increases and equipment upgrades
- Letter to synchrotron facility directors inviting informal proposals
- NIGMS synchrotron advisory group
- FY99 funding of \$7M from NIGMS

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^{*} source Norvell, Aug1999



- > construction of bending magnet beamline
- including beamline optics, monochromator, detector, crystallography station
- > four beamline scientists/technicians
- > \$2,372K equipment/construction
- > \$670K annual staff and operation

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Facility Resources

Optics

Optical element					
	crystal channel cut	energy range	band pass	Intensity	spot size
monochroamtor	Si(111)	6 -23 keV	1.9 x 10 ⁻⁴	1.2 x 10 ¹⁰ ph/s	0.1 x 0.5 mm ²
	coating	figure	magnification	acceptance	
mirror	Rh	Thoroidal	1:1	3mrad	

^{*} I=230 mA, 200 μ m slits at 1.2 Å

Experimental Station



Beamline control:

EPICS / VME

Diffractometer control:

Compumotors

Goniometer control:

Galil

Automounter:

Wago

In line sample viewer:

Wago

Experimental Control, Data Analysis and Storage

Experiment control	1TB RAID 10 system, Dual AMD Opteron 242 Dual Gigabit network	
Data Analysis	twin RAID 10 system	
Data Analysis - Firewall	130GB SCSI Dual Athlon MP	
Backup - Long Term Storage; Data Analysis:	1TB RAID 5 system, Dual AMD Opteron 248 Dual Gigabit network	

Data Collection	BlulCe/DCS	
Data Processing	HKL2000, MOSFLM	
Data Analysis and Refinement	ShelX, CCP4, SOLVE, RESOLVE, CNS,etc	
Model Building	Coot, O	

Crystallization Laboratory

User support:

- Crystallization
- Sample handling
- Cryogenics



Equipment

- Akta Explorer 10 for purification
- Centrifuges
- UV spectrometer
- Fast Gel-system
- Incubators for controlled temperature crystallization
- pH meters, balances



Technical Developments

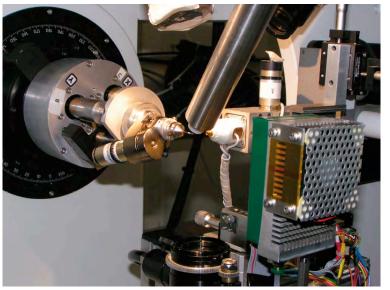


Hardware

- > Fluorescence Detector NSLS
- Beam Position Monitor NSLS
- ➤ Sample in line viewer ALS design
- Sample Illumination NSLS

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Fluorescence Detector - NSLS design

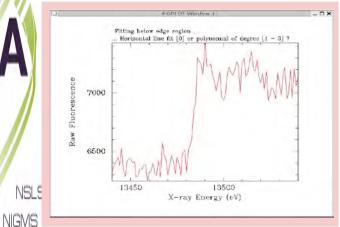


32 element solid state detector

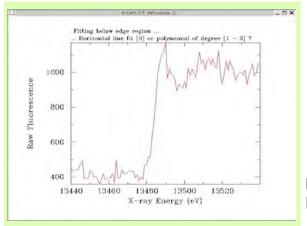
Reasons for replacement of the scintillation detector:

Improved energy resolution,~ 220 eV, ~ 25 eRMS

Improve the measurements of small fluorescence signals



1mg/ml Br solution on a 0.2 mm loop



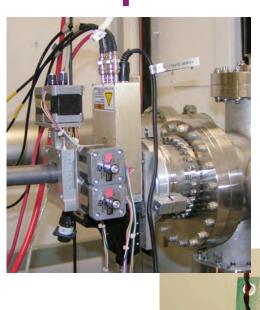
Current Status: >available

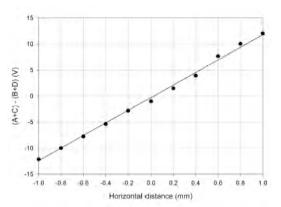
NSLS Control and Detector Group D. P. Siddons, A. Kuczewski

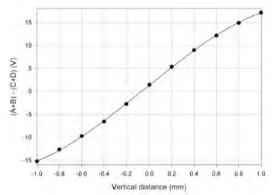
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Scientific Advisory Committee Meeting

Beam position Monitor - NSLS design







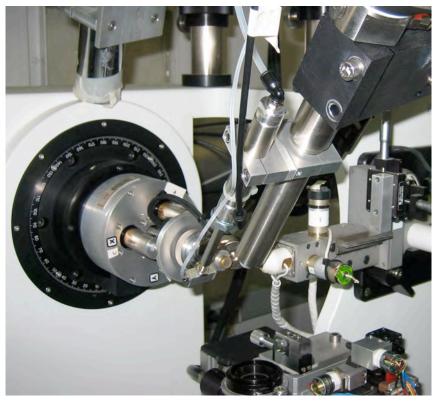
Beam Position Monitor:

- > Replaces Ion Chamber
- > Resolution ~2 microns

Current Status: >available

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In Line Sample Illumination - NSLS design



Improved Sample Illumination:

- Improved contrast
- Automated crystal centering

Current Status:

➤ available

NSLS NIGMS NSLS Control and Detector Group D. P. Siddons, A. Kuczewski NSLS Operation group T. Lenhard

Sample in line viewer - ALS design



ALS Bioinstrumentation Group T. Earnest, E. Cornell, R. Nordmeyer, D. Yoder 19Feb2007

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Reasons for an in-line viewer:

- Sample viewing major complain
- Automated crystal centering

Implementation Strategy:

- Build by the ALS Bio-Instrumentation
- Control software compatible with Blu-Ice like Graphical User Interface/ **Distributed Control System**

Current Status:

- > restricted
- needs to be upgraded

Automated Sample Mounter - ALS design



ALS Bioinstrumentation Group
T. Earnest, E. Cornell, R. Nordmeyer

1500 crystals screened!

- > ~10 groups
- 200 datasets
- > ~ 30 structures in the works

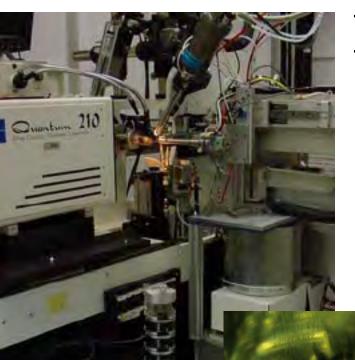
Failures between 1 and 3%! Main Causes:

- Eager users -> command "overload"
- Failure to introduce warm up cycles to the gripper
- Magnet base too strong
- Badly positioned samples in the pucks

Current Status:

Operational

Automated Sample Mounter - ALS design



Two tool sets for users to borrow. Two MOVIES to watch! Requirements:

- will send set (tools + dewar) one week prior to beam time
- set has to be back one week after beam time

Current Status: > Operational

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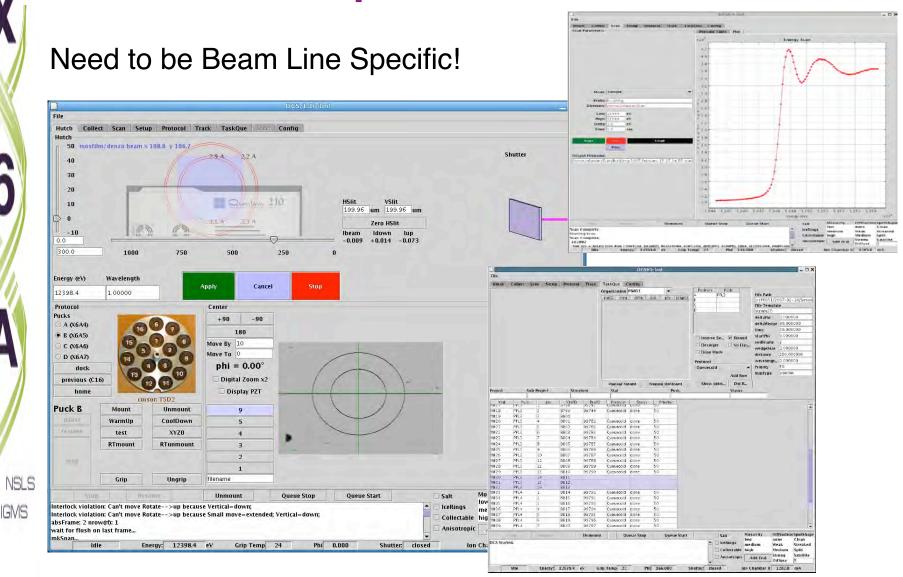
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Software

- Blulce / DCS
- CrysCent
- Crysis

Blulce/DCS - Experimental control



Blulce/DCS - Experimental control

Need to be Beam Line Specific!

- Energy scans
- TaskQue
- Smaller Implementations

Beam sense

Slit adjustment

Key to developments:

- Assistance from Detector and Control Group
- Assistance from Earl Cornell, LBL
- Collaboration with Takeda San Diego Scientists

Current Status:

Operational

CrysCent

Goal: is full automation of the crystal centering process

Follows a "human" Protocol

- Uses machine vision and image processing techniques
- > Is Platform-independent
- > Zero-click, fully automatic crystal centering



Anubhav Jain, Cornell University SULI Program, DOE Submitted

Current Status:

➤ Operational

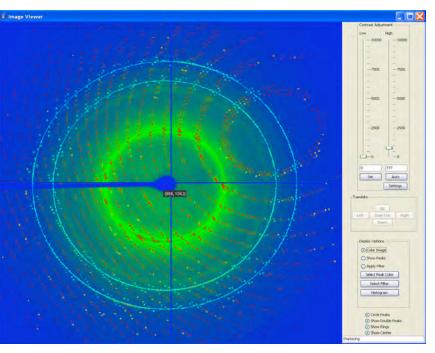
Future Tests:

➤ GM/CA CAT

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CrySis

CrySis (Crystal Analysis) is a software designed to serve as an automated quality control tool for protein crystallography diffraction patterns.



Typical example of Crysis GUI. Shown diffraction peak finding and resolution limit determination screen

Alec Berntson, Cornell University SULI Program, DOE

CrySis

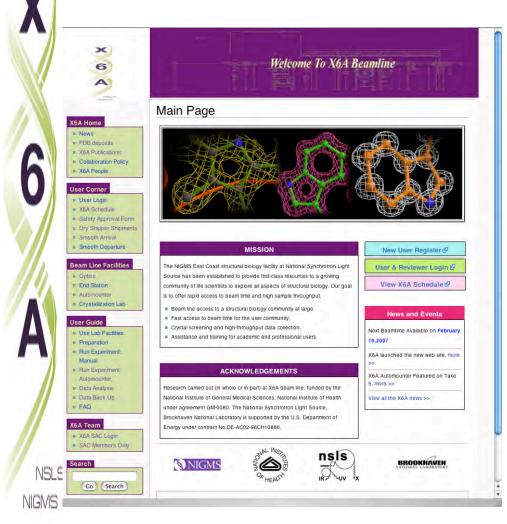
- ➤ Is based on Neural Network algorithms.
- Uses machine vision and image processing techniques
- ➤ Is Platform-independent
- Allows for automated crystal and diffraction quality assessment.

Current Status:

Alec's CS Master Thesis!

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The X6A Web and Database environment



Re-Designed!

Media Wiki

Improve communication

User and Experimental Control Databases

Communication between databases

User Database

- Improve User Access
- Improve Beam Line Management
- Real time Statistical Analysis of beam time usage

The X6A Web and Data Base environment

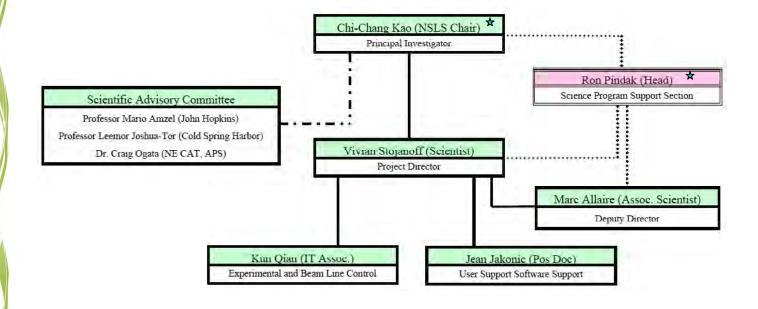
User Database





Staff

Staffing



* NSLS scientific staff

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NSLS Staff contributing to the operation

Technical support provide by the NSLS as needed

Peter Siddons Controls&Detectors

(B. Clay, I. So, Z. Yin, T. Kuczewski)

Steve Hulbert Beamline Support

(S. Cheung, R. Greene, T. Lenhard)

Administrative support provide by the NSLS as needed

Brian Boyle Budget Administration

(W. Morrin)

Eileen Morello Secretarial Support

(A. Bowden)

Katheleen Nasters User Administration

(G. Cisco, L. Flyn, M. Baez)

A. Ackerman EH&S

(J. Aloi)

E. Johnson Operation and Control

B. Kiss Building Management



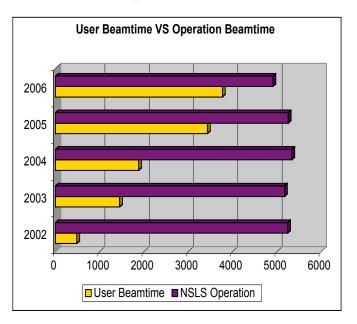
User Program



Two modes are available to users for beam time application:

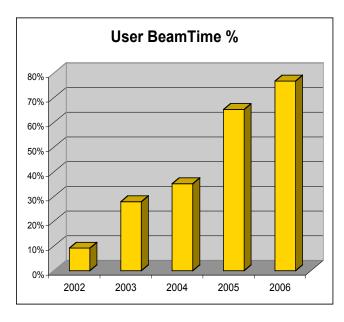
- Program Proposal
 - General User Proposals submitted through the PASS system
 - Multiple projects in one single proposal
- X6A Fast Access (http://protein.nsls.bnl.gov)
 - Projects submitted through the X6A application form
 - Single Projects (1Protein = 1Project)
 - Easy, simple and fast (3 days to a week review process)
 - Multiple visits
 - User schedules own beam time
 - Current Status:
 - Operational
 - Crystal Form Excel spread sheet template to account for automounter operation
 - Integration to the Data Collection Software

X6A Operation: Available Beam



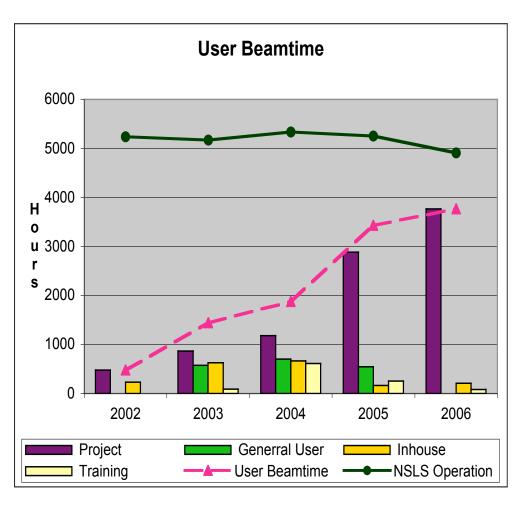
Steady increase in user scheduled beam time reaching saturation

Fully subscribed as 102% of the beam time available to users has been scheduled in 2006.



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User Beam Time



Only one Training Project in calendar year 2006!

X6A was host to Case Center for Proteomics macromolecular users:

18% of NSLS operations

- ➤used 38%
- reverted to X6A 62%
 - ✓Inhouse (18%)
 - ✓X6A user program (60%)
 - ✓ Unused (22%)

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Virtual Users

- Not present during the measurement
- Typically a Fast Access project
- Send in their samples
- Receive image files and scaled data
- Usually also receive an electron density map

Are required to have visited at least once

- > ~ 7 groups sending the samples
- > ~ 6 leaving samples behind

Some were automounter users!



Remote Users

- Not physically present at the facility
- Controls the experiment either assisted by local staff (Video Conferencing) or NoMachine technology with limited staff assistance

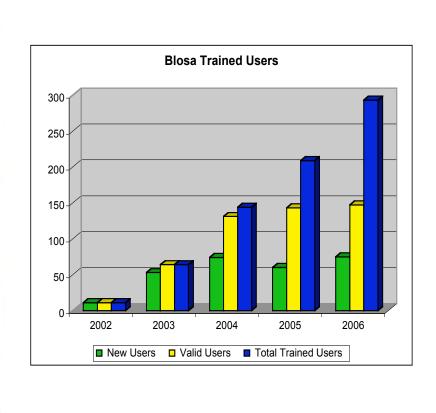
Current status: commissioning

- NoMachine free software installed and tested on beamline computers.
- Successful Data Collection during the Mid Atlantic Macromolecular Crystallography meeting

"Educational" Movie can be downloaded from our web site!

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BLOSA training is valid for two years.

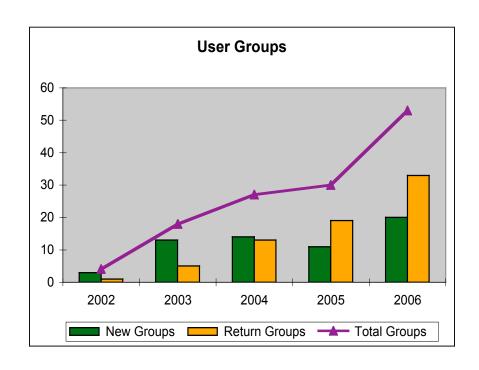
*New Users: are experimenters who got trained in a specific year and were never BLOSA trained in previous years.

*Valid Users: are experimenters who keep a valid BLOSA Training Status in a specific year.

*Total Trained Users: are experimenters who trained in that year or before (accumulated number). Numbers include new and returning users.

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Consolidation of the user community*



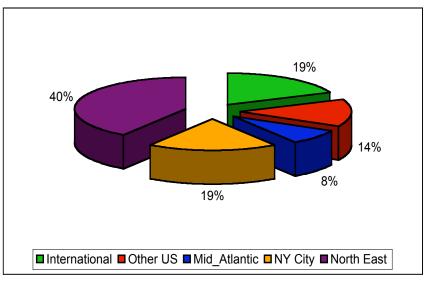
The number of users returning to the beam line has increased significantly in 2006 with 33 returning users and 20 new user groups.

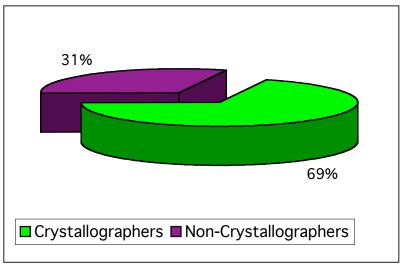
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^{*}Source X6A Survey December 2006

User Group Demographics

59% of all user groups come from academic institutions located in the northeast region of the US.



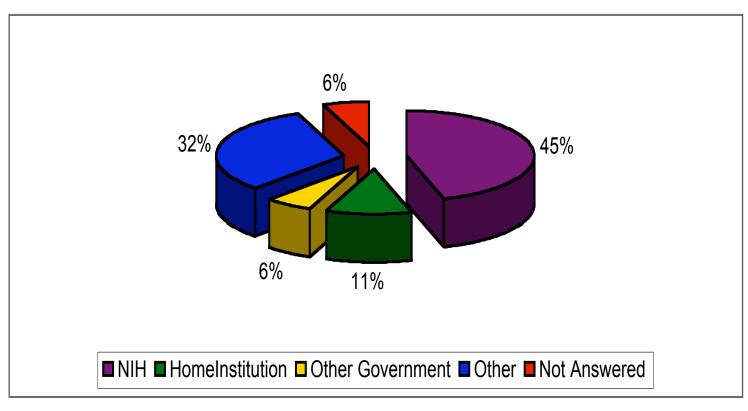


Expert and Non-Expert* user groups.

*numbers are based on project PI's

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Users Funding Sources



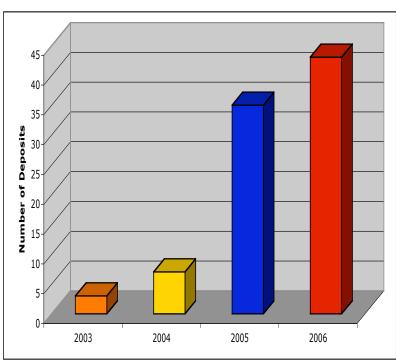
Number of groups supported by the NIH decreased 5% in relation to last year while funding by other sources increased. This is in direct relation to the X6A user base predominantly researchers at the beginning of their careers.

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Impact

Protein Data Bank Deposits*



The number of structures in refinement is larger then the structures released or on hold in 2006. It takes an average of 16 month for users to submit a PDB.

*Source X6A Survey December 2006

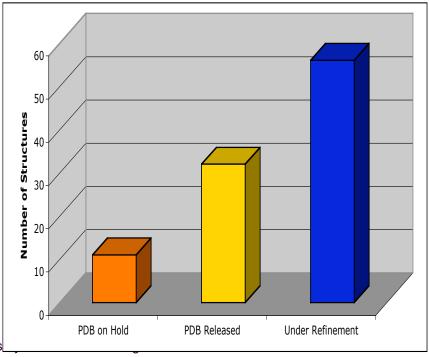
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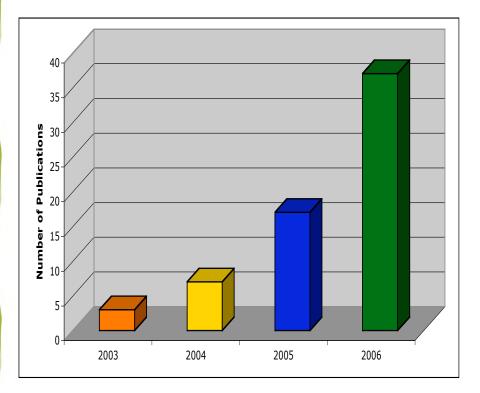
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Scientific Advis

Number of deposits has increased as the beam line is coming to its saturation. The total number of structures related to work performed at the beam line has nearly double in 2006.



Publications*



Publications	
Total	High Impact*
66	29
2006	
37	14

^{*} Journals with an impact of six or greater

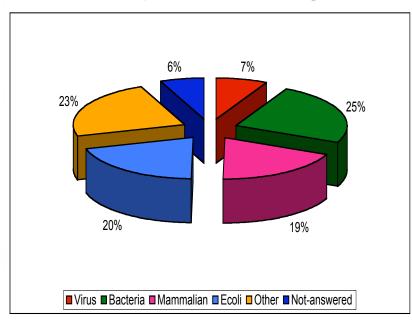
The total number of publications doubled in 2006 with X6A just coming shy of NSLS insertion device beam lines.

*Source X6A Survey December 2006

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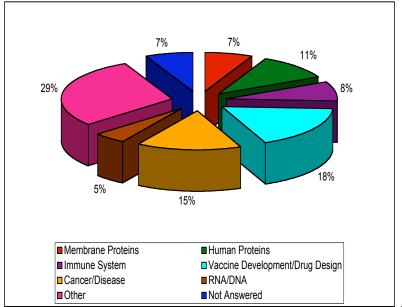
Other Impact Indices*

Projects by Source organism



Projects by Subject Area

64% of the projects developed at the facility focus on topics considered particularly challenging by the NIGMS**

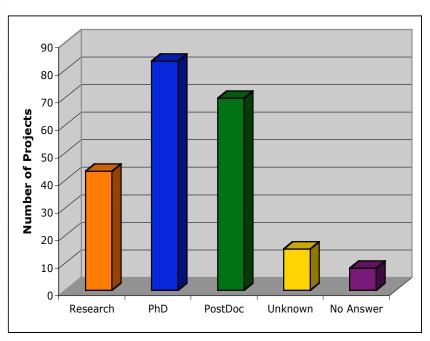


**Source NIGMS FY2006 and 2007 Budget

*Source X6A Survey December 2006

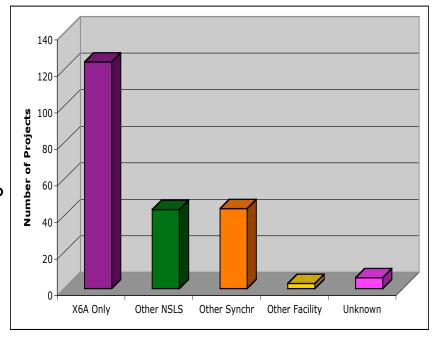
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Other Impact Indices*



More then half of the projects are carried out solely at the Facility, 38% have also used other facilities and further 3% are did not answer to this line item in the survey.

70% of projects developed at the facility support the training of a scientific workforce as reflected by the numbers of PhD and Post-Doctoral research.





Synergy



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Synergy

- > NSLS
- *X4 PRT
 - User beam time re-allocation
 - Technical and scientific approaches to crystallography

PXRR

- X6A users in need of insertion device beam time have been allocated beam time on X29 during their X6A beam time
- Safety Approval Form Streamline
- High pressure freezing facility
- Host for Case Center for Proteomics

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Synergy

With other Synchrotron Facilities

CHESS/MiTeGen
CrysCent autocentering software

>ALS

Distributed Control System: Further developments and functionality implementations, (Thomas Earnest, Carl Cork, Earl Cornell). Automounter feed-back: Christine Tramer (now at SSRL) ??? Sample detection interlock: Christine Tramer (now at SSRL) ???

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Synergy

With other Synchrotron Facilities

>SSRL

Universal puck assembly: testing the universal puck assembly with the X6A sample automounter (A. Cohen, M. Soltis)

Beam line instrumentation: where designs and instrumentation can be shared.

Software development: implementation of web-based user access functionalities; needs careful analysis.

> APS

CrysCent: GM/CA CAT, soft for hard - ware? Automounter dewar: so far the best dewar seems to have been develop by SER CAT. Simulates gravity feed.





FUTURE



Short Term Goals: Technical developments

Improvement of the diffractometer upstream slit assembly:

- Secondary slit box and Helium path
- Upgrade of rotation axis

Automounter:

- Improved lid design
- Reliable autofill system for dewar
- Fully automated sample screening
 - Upgrade of In-line sample viewer

Interlock sample-on and sample-in gripper:

- Sample detection on goniometer head and inside gripper
- Integration with DCS

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- Interlock beam stop:
 - Detection of beam stop in position
 - Integration with DCS



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Short Term Goals: User program

Beam Time Access:

- Provide a user friendly environment as many experimenters are first time synchrotron users;
- Consolidation of Virtual User, staff assisted sample automounter use;
- Encourage Remote access



- Strong research program with good alignment with NIGMS mission.
- Young Faculty User base.
- Upgrade of Internet Services facilitates User access to beam time and Facility management.
- ➤ Inhouse development of software and beam line instrumentation increase data collection efficiency.
- ➤ Increased beam line productivity has been noticeable in 2006.
- NBLS > Good synergy with other Facilities.

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